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(71) Applicant: SCHERING CORPORATION [US/US]; 2000 Galloping Hill Road, Kenilworth, NJ 07033 (US).

(72) Inventors: ZURAWSKI, Sandra, M.; 1028 Wilmington Way, Redwood City, CA 94062 (US). ZURAWSKI, Gerard; 1028 Wilmington Way, Redwood City, CA 94062 (US).

(74) Agents: FOULKE, Cynthia, L. et al.; Schering-Plough Corporation, Patent Dept. K-6-1 1990, 2000 Galloping Hill Road, Kenilworth, NJ 07033-0530 (US).

(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG).

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(54) Title: MUTEINS OF MAMMALIAN CYTOKINES

(57) Abstract

Methods for screening for partial agonists and for antagonists of mammalian cytokines. Particular positions of natural cytokines are identified as critical in providing these receptor mediated properties. Specific embodiments demonstrate properties of variations at these positions.

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INTERNATIONAL SEARCH REPORT

Inte·~onal Application No
PCT/US 95/08950

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/26 C12N15/24 C07K14/55 G01N33/68 C07K14/54
A61K38/20

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 262, no. 12, 25 April 1987 MD US, pages 5723-5731, G. JU ET AL 'Structure-function analysis of human interleukin-2: Identification of amino acid residues required for biological activity ' see the whole document especially figure 3 see page 5726, right column ---	1-6,9,10
X	BIOTECHNOLOGY, vol. 7, no. 7, July 1989 NEW YORK US, pages 716-720, J.F. ERNST ET AL 'Screening of muteins secreted by yeast: Random mutagenesis of human interleukin-2' see page 719 ---	1,2,4,5

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
13 February 1996	20.02.96

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	Le Cornec, N

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PROTEINS: STRUCTURE, FUNCTION, AND GENETICS, vol. 9, no. 3, March 1991 pages 207-216, B.E. LANDGRAF ET AL 'Conformational perturbation of Interleukin-2 : A strategy for the design of cytokine analogs' see page 209, right column, paragraph 3 see page 210; figure 1 see page 211, right column, paragraph 2 see page 212, left column, paragraph 1 see page 212, right column; figures 4-6 see page 215, right column, line 30 - line 36 ---	1,3,9,10
X	EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 180, 1989 pages 295-300, U. WEIGEL ET AL 'Mutant proteins of human interleukin-2' see page 298, left column; figure 3 ---	1,9,10
A	EMBO JOURNAL, vol. 9, no. 12, 1990 EYNSHAM, OXFORD GB, pages 3899-3905, S. M. ZURAWSKI ET AL 'Partial agonist/antagonist mouse interleukin-2 proteins indicate that a third component of the receptor complex functions in signal transduction ' see the whole document ---	1-10
A	SCIENCE, vol. 257, 17 July 1992 LANCASTER, PA US, pages 410-413, J.F. BAZAN AND D.B. MCKAY 'unraveling the structure of iL-2' cited in the application ---	
A	JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 264, no. 2, 15 January 1989 MD US, pages 816-822, B. LANDGRAF EET AL 'Structural significance of the C-terminal amphiphilic helix of interleukin-2' see the whole document ---	1
X	JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 251, no. 1, 1986 MD US, pages 334-337, S.M. LIANG ET AL 'Studies of structure-activity relationships of human interleukin-2' see page 336; table III ---	1,2,9

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/08950

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO,A,90 00565 (AMGEN INC.) 25 January 1990 ---	
A	US,A,5 229 109 (E.A. GRIMM ET AL) 20 July 1993 see the whole document -----	1

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/08950

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: 10
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 10 (as far as it does not concern in vitro methods) is directed to a method of treatment of the human/animal body (Rule 39.1(iv) PCT)), the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. claims 1-10 (see also "remark")
2. claims 11-19
3. claim 20, partially
4. claim 20, partially
5. claim 20, partially (See additional sheet PCT/ISA/210)

1. [ ] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. [ ] As all searchable claims could be searches without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-10

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

1. claims 1-10: Mutein of human IL-2, DNA encoding it and use of the mutein in a pharmaceutical composition
2. claims 11-19: Mutein of human IL-13 and mouse P600, DNA encoding it and use of the mutein in diagnostics
3. claim 20 : Mutein of mammalian interleukin-7
4. claim 20 : Mutein of mammalian interleukin-9
5. claim 20 : Mutein of mammalian interleukin-15

INTERNATIONAL SEARCH REPORT

Information on patent family members

Intr   ·onal Application No
PCT/US 95/08950

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO-A-9000565	25-01-90	AU-B-	627477	27-08-92
		AU-B-	3877689	05-02-90
		EP-A-	0378666	25-07-90
		JP-T-	3500415	31-01-91
US-A-5229109	20-07-93	AU-B-	4284393	18-11-93
		EP-A-	0673257	27-09-95
		JP-T-	7508714	28-09-95
		WO-A-	9320849	28-10-93

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(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG).

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MUTEINS OF MAMMALIAN CYTOKINES

FIELD OF THE INVENTION

The present invention relates to compositions which include variants of human cytokines which function in controlling development and differentiation of mammalian cells, e.g., cells of a mammalian immune system. In particular, it provides antagonists of proteins which regulate development, differentiation, and function of various cell types, including hematopoietic cells.

BACKGROUND OF THE INVENTION

The circulating component of the mammalian circulatory system comprises various cell types, including red and white blood cells of the erythroid or the myeloid cell lineages. See, e.g., Rapaport (1987) Introduction to Hematology (2d ed.) Lippincott, Philadelphia, PA; Jandl (1987) Blood: Textbook of Hematology, Little, Brown and Co., Boston, MA.; and Paul (ed.)(1993) Fundamental Immunology (3d ed.), Raven Press, N.Y. Myeloid cell production occurs through the differentiation and later commitment of myeloid progenitor cell lineages.

In addition, functional interaction of the various cell types involved in immune responses often involve transfer of signals via soluble messenger molecules. The cytokines and lymphokines are molecules which mediate differentiation or other signals, typically between cells. Cytokines function through receptors, many of which have been characterized. See, e.g., Aggarwal and Gutterman (eds.) (1991) Human Cytokines: Handbook for Basic and Clinical Research, Blackwell, Oxford. As the cytokines are so important in development and regulation of immune responses, the inability to modulate these signals has prevented means to intervene in abnormal physiological or developmental situations. The present invention addresses these problems and provides various molecules which are useful in these situations.

SUMMARY OF THE INVENTION

The present invention provides molecules which can serve as an agonist or antagonist for various cytokines. These agonists and antagonists will be useful in diagnosis of cytokine or cytokine receptor levels. In certain circumstances, these molecules will also have in vitro or in vivo therapeutic effects.

The present invention is based, in part, upon the discovery of which specific amino acid residues of a cytokine are important in the binding and signal transduction components of cytokine-receptor binding. It embraces various mutein agonists and antagonists of the natural ligands, e.g., specific mutations (muteins) of the natural sequences, fusion proteins, and chemical mimetics. It is also directed to DNAs encoding such proteins. Various uses of these different protein or nucleic acid compositions are also provided.

The present invention provides a mutein of a human IL-2, said mutein exhibiting both:

1) partial cytokine agonist activity; and
2) a substitution in the sequence at a position:
   a) between helix B and helix C; or
   b) in helix D.

In particular embodiments, the muteins has a sequence of:

1) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCqSIIS TLT;
2) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCETADE TATIVEFLNR WITFCqSIIS TLT; or
3) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCETADE TATIVEFLNR WITFsqSIIS TLT.

The mutein can also exhibit less than 80% maximal agonist activity of natural IL-2; and/or at a 1000-fold excess antagonizes cytokine agonist activity by at least about 50%. In particular embodiments, the mutein exhibits a substitution:

1) at a position between helix B and helix C which corresponds to position 82 (pro) of a hydrophobic amino acid, including alanine, and/or
2) at a position in helix D which corresponds to position 126 (gln) of an acidic amino acid, including aspartic acid.

The mutein can also contain substitutions at position 82 (pro) and/or 126 (gln).

The invention also embraces a pharmaceutical composition comprising such mutein and a pharmaceutically acceptable carrier or excipient; a nucleic acid encoding these muteins; and methods of antagonizing biological activity of IL-2 on a cell comprising contacting the cell with such a mutein.

The invention also provides a mutein of a cytokine selected from:

1) a human IL-13, the mutein exhibiting both:
    a) partial agonist activity; and
    b) a substitution in sequence at positions corresponding to:
        i) a position in helix A; and/or
        ii) a position in helix C; and
2) a mouse P600, the mutein exhibiting both:
    a) partial agonist activity; and
    b) a substitution in sequence at a position in helix C.

In various embodiments, the human IL-13 has a sequence of:

i) GPVPPSTALR eLIEELVNIT QNQKAPLCNG SMVWSINLTA GMYCSAAALE SLINVSGCIE KTQrMLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL HLKKLFRGRFN; or
ii) GPVPPSTALR eLIEELVNIT QNQKAPLCNG SMVWSINLTA GMYCSAAALE SLINVSGCIE KTQrMLSGFC PHKVSAG-FS SLHVRDTKIE VAQFVKDLLL HLKKLFRGRFN; or

the mouse P600 has a sequence of GPVPRSVSLP LTLKELIEEL VNITQDETPL CNGSMVWSVD LAAGGFCNAV ALDSLTNISN CIYRTQrILH GLCNRKAPTT VSSLPDTKIE VAHFITKLLS YTKQLFRHGP F. Preferably, these muteins exhibit less than 80% maximal agonist activity;

and/or at a 100-fold excess antagonizes cytokine activity by at least 50%. In various embodiments, the position of:

1) human IL-13 in:
   a) helix A corresponds to position 11 (gly); and/or
   b) helix C corresponds to position 64 (arg); or
2) mouse P600 in helix C corresponds to position 67 (arg).

In particular embodiments, the substitution of human IL-13 is:

a) an aminated amino acid, including lysine, at position 11 (gly); and/or
b) an acidic amino acid, including aspartic acid, at position 64 (arg); or

the substitution of mouse P600 is an acidic amino acid, including aspartic acid, at position 67 (arg). The invention also encompasses a nucleic acid encoding these muteins; methods of antagonizing biological activity of IL-4 or IL-13 on a cell by contacting the cell with such muteins; and methods of analyzing human IL-13 or mouse P600 by measuring antagonistic activity of such muteins in an assay.

In yet another embodiment, the present invention provides a mutein of a mammalian cytokine selected from the group consisting of:

1) IL-7;
2) IL-9; and
3) IL-15;

said mutein exhibiting both:

1) partial agonist activity; and
2) a substitution in the sequence at a position corresponding to a position in:
   a) IL-7 or IL-9 in between helix B and helix C; and/or helix D; or
   b) IL-15 in helix A and/or helix C.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows effects of various muteins of mouse IL-2 on HT2 cells (see Zurawski, et al. (1986) J. Immunol. 137:3354-3360). Panel A shows antagonist activity of mouse IL-2 mutein Q141D. Abscissa: -log [mIL-2.Q141D] in Molar units; ordinate: OD (570 - 650 nm). The $I_{50} = 2 \times 10^{-9}$ M. Assays used 100 µl per well, 10^4 cells per well. Panel B shows partial agonist activities on HT2 cells of various muteins of mouse IL-2, in particular, native, Q141K, Q141V, Q141L, and Q141D. Abscissa: -log [mIL-2 protein] in Molar units; ordinate: OD (570 - 650 nm). Positions corresponding D34, N99, and N103 in human IL-2 are predicted to be important. Similarly, in human IL-4, R88 (within the sequence of KDTRCLG) should be important.

Figure 2 shows partial agonist and antagonist activity of human IL-2 mutein P82A;Q126D on mouse Baf3 cells (see Imler, et al. (1992) EMBO J. 11:2047-2053). Panel A shows almost complete lack of agonist activity on mouse Baf3 cells cotransfected with both the α and β subunits of the human IL-2 receptor (see Izuhara, et al. Biochem. Biophys. Res. Comm. 190:992-1000). Abscissa: -log [hIL-2.P82A;Q126D] in Molar units; ordinate: OD (570 - 650 nm). Panel B shows dose response curve of human IL-2 in the absence or presence of 2×10^{-7} M IL-2 mutein. Abscissa: -log [hIL-2 protein] in Molar units; ordinate: OD (570 - 650 nm). Other important target residues in the human IL-2 include L94 and E95.

Figure 3 shows partial agonist and antagonist activity of human IL-13 mutein E11K;R64D on TF-1 cells. Panel A shows partial agonist activity of this hIL-13 mutein. Abscissa: -log [hIL-13.E11K;R64D] in Molar units; ordinate: OD (570 - 650 nm). Panel B shows dose response curve of human IL-13 in the absence or presence of 5×10^{-8} M IL-13 mutein. Abscissa: -log [hIL-13 protein] in Molar units; ordinate: OD (570 - 650 nm). Position K61 of human IL-13 may also be important.

Figure 4 shows partial agonist and antagonist activity of mouse IL-13 mutein R67D on B9 cells (see Brackenhoff, et al. (1994) J. Biol. Chem. 269:86-93). Panel A shows partial agonist

activity of mouse IL-13 mutein R67D on B9 cells. Abscissa: -log [mIL-13.R67D] in Molar units; ordinate: OD (570 - 650 nm). Panel B shows dose response curve of mouse IL-13 in the absence or presence of 5 x 10^{-7} M IL-13 mutein.. Abscissa: -log [mIL-13 protein] in Molar units; ordinate: OD (570 - 650 nm).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. General

Extensive research has suggested that one cell communicates with another cell through discrete chemical molecules known as cytokines. Involvement of cytokines in a wide variety of diseases has been found, including cancer, allergy, infection, inflammation, wound healing, angiogenesis, differentiation, morphogenesis, and embryogenesis.

The present invention provides sequence variants of cytokines, e.g., muteins, which serve as antagonists of the cytokines. The natural ligands are capable of mediating various biochemical responses which should lead to biological or physiological responses in target cells, e.g., as described above.

Physically, relevant cytokines have been described, as shown in Table 1. The table provides the GenBank accession numbers of each cytokine, and references providing gene and/or cytokine amino acid sequence. Many receptor sequences are also available from GenBank. See also Howard, et al. (1993) in Paul (ed.) (1993) Fundamental Immunology (3d ed.) Raven Press, NY.

Table 1. Cytokines and references.

cytokine	GenBank #	Reference
mGM-CSF	X03221	Gough, et al. (1984) Nature 309:763-767
hGM-CSF	M6445	Lee, et al. (1985) PNAS 82:4360-4364; Wong, et al. (1985) Cancer Cells 3:235-242
mIL-2	M16760-62	see Arai, et al. (1990) Ann. Rev. Biochem. 59:783-836
hIL-2	J00264	Fujita, et al. (1983) PNAS 80:7437-7441
mIL-3	K03233	Fung, et al. (1984) Nature 307:233-237
hIL-3	M14743 M20137 M33135	Yang, et al. (1986) Cell 47:3-10

mIL-4	M29854	Howard, et al. (1984) Immunol. Revs. 78:185-210; Swain, et al. (1983) J. Expt'l Med. 158:822-835
hIL-4	M13982	Yokota, et al. (1986) PNAS 83:5894-5898
mIL-5	X06270	Kinashi, et al. (1986) Nature 324:70-73
hIL-5	X04688	Kinashi, et al. (1986) Nature 324:70-73
mIL-7	X07962	Lupton, et al. (1990) J. Immunol. 144:3592-3601
hIL-7	J04156	Lupton, et al. (1990) J. Immunol. 144:3592-3601
mIL-9	X14045	Van Snick, et al. (1989) J. Expt'l Med. 169:363-372
hIL-9	X17543 M30134	Yang, et al. (1989) Blood 74:1880-1884; Renauld, et al. (1990) J. Immunol. 144:4235-4243
IL-15	U03099	Grabstein, et al. (1994) Science 264:965-968

Corresponding bioassays are described, e.g., in Aggarwal and Gutterman (eds.) (1991) Human Cytokines: Handbook for Basic and Clinical Research, Blackwell, Oxford. These assays are useful in screening for partial agonist or antagonist activities.

Typical IL-2 bioassay: see Gillis, et al. (1978) J. Immunol. 120:2027-2031.

Typical IL-3 bioassay: growth of IL-3 responsive cells; see Lange, et al. (1987) Blood 70:192-199; Avanzi, et al. (1988) Br. J. Haematol. 69:359-366. This cytokine also exhibits growth and differentiation effects on neutrophils, macrophages, megakaryocytes, erythrocytes, eosinophils, basophils, and mast cells; stimulates the function of mature mast cells, basophils, eosinophils, and macrophages.

Typical IL-4 assays: see Spits, et al. (1987) J. Immunol. 139:1142-1147. This cytokine also exhibits effects on T cells, thymocytes, Natural Killer (NK) cells, Lymphocyte Activated Killer (LAK) cells, B cells, Burkitt's Lymphoma cells, B cell lymphomas, monocytes, hematopoietic precursor cells, eosinophils, neutrophils, and endothelial cells.

Typical IL-5 assays: see Kitamura, et al. (1989) J. Cell. Physiol. 140:323-334. This cytokine also exhibits effects on T cells, B cells, hematopoietic progenitor cells, and eosinophils.

Typical IL-7 assays: effects on IL-7 responsive cells, see Namen, et al. (1988) Nature 333:571-573; Sudo, et al. (1989) J. Expt'l Med. 170:333-338. This cytokine also exhibits effects on B cell progenitors and thymocytes.

Typical IL-9 assays: see Yang, et al. (1989) Blood 74:1880-1884; Renauld, et al. (1990) J. Immunol. 144:4235-4243.

Typical IL-13 assays: described, e.g., in Minty, et al. (1993) Nature 362:248-250; and McKenzie, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:3735-3739; and see Zurawski and de Vries (1994) Immunol. Today 15:19-26.

Typical IL-15 assays: see Grabstein, et al. (1994) Science 264:965-968.

For the assays described herein, typically one finds a cell line whose growth is factor dependent and specific for a desired cytokine. Exemplary cell lines are: for mouse GM-CSF, NFS60 (see Holmes, et al. (1985) Proc. Nat'l Acad. Sci. USA 82:6687-6691); for human GM-CSF, use TF-1; for mouse IL-2, use HT2 cells; for human IL-2, use Kit225 cells or mouse Baf3 cells transformed with human IL-2R subunits $\alpha$and β; for mouse IL-3, use NFS60; for human IL-3, use TF-1; for mouse IL-4, use HT2 cells; for human IL-4, use TF-1 cells; for mouse IL-5, use NFS60; for human IL-5, use TF-1; for human IL-7, use thymocyte cell lines; for human IL-9, use M07E cells, see Yang, et al. (1989) Blood 74:1880-1884; for both mouse and human IL-13, use TF-1 cells; for IL-15, use YT cells, see Yodoi, et al. (1985) J. Immunol. 134:1623-1630.

With a selected cell line, a dose-response curve of the appropriate cytokine is performed. This gives a plateau, or maximal stimulation at saturating or excess amounts of cytokine. Typically, the cytokine will show a useful dose-response in the range of 10^{-7} to 10^{-13} M cytokine. The half maximal response typically will fall in the range of 10^{-9} to 10^{-12} M.

A mutein candidate agonist is tested, preferably with a sequence substitution as described, by titrating a dose response curve of the cytokine in the absence or presence of the candidate mutein at a fixed concentration. Typically the

candidate mutein concentration is fixed, preferably within the range of equimolar to the half-maximum of the target cytokine, or at a 10-, 100-, or 1000- fold excess of candidate mutein over that half-maximum amount. Typically, the dose response curve of the cytokine will shift. The shift will normally be at least one log unit, often two to four log units.

To test partial agonist activity of the candidate mutein, a dose-response curve of the mutein is performed. Typically, the maximal stimulatory activity of the mutein will be near that of the natural cytokine, but partial agonists will show a suboptimal stimulation at saturation, e.g., the maximal activity will plateau at a lesser amount. This amount will often be less than about 90%, preferably less than about 75%, more preferably less than about 50%, and in most preferred embodiments, even less than about 25%. Agonists with an even lesser maximum will still be useful, and often provide the most promising candidates for establishing chemical antagonist properties.

Specific analyses for IL-2 and IL-13 are shown in the figures. Similar analysis can be performed with the GM-CSF, IL-3, and IL-5 series of muteins. These three cytokines share similarities in their receptor behavior due, in part, to sharing of receptor structures. Similarities also exist for IL-7, IL-9, and IL-15, due also, apparently, to shared receptor structures.

Muteins are made typically by site specific mutagenesis of natural cytokine at defined positions. The sequences of the cytokines are referred to in Table 1, GenBank, and the references cited therein. Initially, single and low multiplicity mutagenesis will be constructed, with more complex combinations also available. The tertiary structural features of the cytokines have been described, e.g., in Bazan (1991) Cell 66:9-10; Bazan (1990) Immunology Today 11:350-354; Bazan (1992) Science 257:410-413; Rozwarski, et al. (1994) Structure 2:159-173; and Sprang and Bazan (1993) Current Opinion in Structural Biology 3:815-827. These references define common structural features of the cytokines, e.g., the helices A, B, C, and D therein, including sequence alignments and corresponding

positions. See also Zurawski, et al. (1993) EMBO J. 12:2663-2670. The specific positions of critical substitutions typically are conserved across different cytokines in various patterns, and because the helical turn involves 3.5 residues per turn, 3 or 4 residues and 7 residues in either direction will be positioned adjacent on the surface of a cytokine.

II. Agonists; antagonists

The process of inhibition or prevention of agonist-induced responses is termed antagonism, and chemical entities with such properties are antagonists. See, e.g., Kenakin (1987) Pharmacological Analysis of Drug-Receptor Interaction Raven Press, NY.

Various classes of antagonists include chemical or neutralization antagonists, competitive antagonists, and noncompetitive antagonists. The chemical or neutralization antagonists interact with the agonist and prevent activation of the receptor and subsequent response, e.g., antibody antagonists which bind to the agonist and block signaling thereby.

The competitive antagonists are molecules which bind to the same recognition site on the receptor and block agonist binding. Noncompetitive antagonists bind to a site on the receptor distinct from the agonist binding site, and block signal transduction.

Measurement of antagonist activity and analysis of these results can be performed by Schild analysis. See Arunlakshana and Schild (1959) Br. J. of Pharmacol. 14:48-58; and Chapter 9 of Kenakin (1987) Pharmacological Analysis of Drug-Receptor Interaction Raven Press, NY. See also Black (1989) Science 245:486-493. Schild analysis with a defined antagonist provides a number of means to evaluate quantity and quality of both agonist and receptor preparations. For example, analysis of a preparation of agonist allows better quality control indications than ELISA or mere bioassay quantitation methods. It provides means to distinguish between a denatured agonist, which is more

likely to test positive in ELISA assays, and a biologically active agonist.

The described muteins are typically proteinaceous, though a full length is not necessary. Fragments can be useful where they include positions which have been mutated as provided herein.

The term "polypeptide" as used herein includes a significant fragment or segment, and encompasses a stretch of amino acid residues of at least about 8 amino acids, generally at least about 12 amino acids, typically at least about 16 amino acids, preferably at least about 20 amino acids, and, in particularly preferred embodiments, at least about 30 or more amino acids. Virtually full length molecules with few substitutions will be preferred in most circumstances.

Substantially pure typically means that the mutein is free from other contaminating proteins, nucleic acids, and other biologicals derived from the original source organism. Purity may be assayed by standard methods, typically by weight, and will ordinarily be at least about 40% pure, generally at least about 50% pure, often at least about 60% pure, typically at least about 80% pure, preferably at least about 90% pure, and in most preferred embodiments, at least about 95% pure.

The size and structure of the polypeptide should generally be in a substantially stable state, and usually not in a denatured state. The polypeptide may be associated with other polypeptides in a quaternary structure, e.g., to confer solubility, or associated with lipids or detergents in a manner which approximates natural lipid bilayer interactions.

The solvent and electrolytes will usually be a biologically compatible buffer, of a type used for preservation of biological activities, and will usually approximate a physiological aqueous solvent. Usually the solvent will have a neutral pH, typically between about 5 and 10, and preferably about 7.5. On some occasions, one or more detergents will be added, typically a mild non-denaturing one, e.g., CHS or CHAPS, or a low enough

concentration as to avoid significant disruption of structural or physiological properties of the ligand.

III. Physical Variants

This invention also encompasses proteins or peptides having sequence variations at positions corresponding to the specified residues, but with substantial amino acid sequence identity at other segments. The variants include species variants and particularly molecules with the same primary sequence but variations beyond primary amino acid sequence, e.g., glycosylation or other modifications.

Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches, if necessary, by introducing gaps as required. See also Needleham, et al. (1970) J. Mol. Biol. 48:443-453; Sankoff, et al. (1983) Chapter One in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group, Madison, WI;. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Substitutions at designated positions can often be made with homologous residues to retain similar activities, e.g., agonist or antagonist functions. Identity measures will be at least about 85%, usually at least about 95%, preferably at least about 97%, and more preferably at least 98% or more, especially about the particular residue positions identified as appropriate for sequence changes. Regions of particular importance are within about 5 amino acids surrounding the defined positions, more particularly within about 8 amino acids, and preferably within about 11 amino acids adjacent the positions where changes are indicated.

The isolated cytokine DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide

insertions, and inversions of nucleotide stretches. These modifications result in novel DNA sequences which encode these proteins having many similar physiological, immunogenic, antigenic, or other functional activity. Enhanced expression may involve gene amplification, increased transcription, increased translation, and other mechanisms.

Cytokine mutagenesis can also be conducted by making amino acid insertions or deletions. Substitutions, deletions, insertions, or any combinations may be generated to arrive at a final construct. Insertions include amino- or carboxy- terminal fusions. Random mutagenesis can be conducted at a target codon and the expressed mutants can then be screened for the desired activity. Methods for making substitution mutations at predetermined sites in DNA having a known sequence are well known in the art, e.g., by M13 primer mutagenesis or polymerase chain reaction (PCR) techniques. See, e.g., Sambrook, et al. (1989); Ausubel, et al. (1987 and Supplements); and Kunkel, et al. (1987) Meth. Enzymol. 154:367-382.

The present invention also provides recombinant proteins, e.g., heterologous fusion proteins using segments from these proteins. A heterologous fusion protein is a fusion of proteins or segments which are naturally not normally fused in the same manner. A similar concept applies to heterologous nucleic acid sequences.

In addition, new constructs may be made from combining similar functional domains from other proteins. For example, ligand-binding or other segments may be "swapped" between different new fusion polypeptides or fragments. See, e.g., Cunningham, et al. (1989) Science 243:1330-1336; and O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA

polymerase with an appropriate primer sequence, e.g., PCR techniques.

"Derivatives" of these cytokines include amino acid sequence mutants at other positions remote from those specified, glycosylation variants, and covalent or aggregate conjugates with other chemical moieties. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in amino acid side chains or at the N- or C- termini, by standard means. See, e.g., Lundblad and Noyes (1988) Chemical Reagents for Protein Modification, vols. 1-2, CRC Press, Inc., Boca Raton, FL; Hugli (ed.) (1989) Techniques in Protein Chemistry, Academic Press, San Diego, CA; and Wong (1991) Chemistry of Protein Conjugation and Cross Linking, CRC Press, Boca Raton, FL.

In particular, glycosylation alterations are included, e.g., made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing, or in further processing steps. See, e.g., Elbein (1987) Ann. Rev. Biochem. 56:497-534. Also embraced are versions of the peptides with the same primary amino acid sequence which have other minor modifications, including phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

Fusion polypeptides between these cytokine muteins and other homologous or heterologous proteins are also provided. Many growth factors and cytokines are homodimeric entities, and a repeat construct may have various advantages, including lessened susceptibility to proteolytic cleavage. Typical examples are fusions of a reporter polypeptide, e.g., luciferase, with a segment or domain of a ligand, e.g., a receptor-binding segment, so that the presence or location of the fused ligand may be easily determined. See, e.g., Dull, et al., U.S. Patent No. 4,859,609. Other gene fusion partners include bacterial ß-galactosidase, trpE, Protein A, ß-lactamase, alpha amylase, alcohol dehydrogenase, and yeast alpha mating factor. See, e.g., Godowski, et al. (1988) Science 241:812-816.

Fusion peptides will typically be made by either recombinant nucleic acid methods or by synthetic polypeptide methods. Techniques for nucleic acid manipulation and expression are described generally, e.g., in Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), vols. 1-3, Cold Spring Harbor Laboratory; and Ausubel, et al. (eds.) (1993) Current Protocols in Molecular Biology, Greene and Wiley, NY. Techniques for synthesis of polypeptides are described, e.g., in Merrifield (1963) J. Amer. Chem. Soc. 85:2149-2156; Merrifield (1986) Science 232: 341-347; and Atherton, et al. (1989) Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford; and Grant (1992) Synthetic Peptides: A User's Guide, W.H. Freeman, NY.

This invention also contemplates the use of derivatives of these cytokine muteins other than variations in amino acid sequence or glycosylation. Such derivatives may involve covalent or aggregative association with chemical moieties. Covalent or aggregative derivatives will be useful as immunogens, as reagents in immunoassays, or in purification methods such as for affinity purification of receptors or other binding ligands. A cytokine mutein can be immobilized by covalent bonding to a solid support such as cyanogen bromide-activated SEPHAROSE, by methods which are well known in the art, or adsorbed onto polyolefin surfaces, with or without glutaraldehyde cross-linking, for use in the assay or purification of anti-cytokine antibodies or its receptor. The cytokine muteins can also be labeled with a detectable group, for use in diagnostic assays. Purification of cytokine muteins may be effected by immobilized antibodies or receptor.

The present invention contemplates corresponding muteins the isolation of additional closely related species variants, e.g., rodents, lagomorphs, carnivores, artiodactyla, perissodactyla, and primates.

~~The invention also provides means to isolate a group of~~ related muteins displaying both distinctness and similarities in structure, expression, and function. Elucidation of many of the

physiological effects of the muteins will be greatly accelerated by the isolation and characterization of distinct species variants.

The isolated genes encoding muteins will allow transformation of cells lacking expression of a corresponding cytokine, e.g., either species types or cells which exhibit negative background activity.

Dissection of critical structural elements which effect the various receptor mediated functions provided by cytokine binding is possible using standard techniques of modern molecular biology, particularly in comparing members of the related class. See, e.g., the homolog-scanning mutagenesis technique described in Cunningham, et al. (1989) Science 243:1339-1336; and approaches used in O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992; and Lechleiter, et al. (1990) EMBO J. 9:4381-4390.

IV. Nucleic Acids

The described peptide sequences are readily made by expressing a DNA clone encoding the mutein, e.g., modified from a natural source. A number of different approaches should be available to successfully produce a suitable nucleic acid clone.

The purified protein or defined peptides are useful as described above. Synthetic peptides or purified protein can be presented to an immune system to generate monoclonal or polyclonal antibodies which recognize specifically the muteins. See, e.g., Coligan (1991) Current Protocols in Immunology Wiley/Greene; and Harlow and Lane (1989) Antibodies: A Laboratory Manual, Cold Spring Harbor Press.

This invention contemplates use of isolated DNA or fragments to encode a biologically active corresponding mutein. In addition, this invention covers isolated or recombinant DNA which encodes a biologically active antagonist or partial agonist protein or polypeptide.

An "isolated" nucleic acid is a nucleic acid, e.g., an RNA, DNA, or a mixed polymer, which is substantially separated from

other components which naturally accompany a native sequence, e.g., ribosomes, polymerases, and flanking genomic sequences from the originating species. The term embraces a nucleic acid sequence which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates and chemically synthesized analogs or analogs biologically synthesized by heterologous systems. A substantially pure molecule includes isolated forms of the molecule. Generally, the nucleic acid will be in a vector or fragment less than about 50 kb, usually less than about 30 kb, typically less than about 10 kb, and preferably less than about 6 kb.

An isolated nucleic acid will generally be a homogeneous composition of molecules, but will, in some embodiments, contain minor heterogeneity. This heterogeneity is typically found at the polymer ends or portions not critical to a desired biological function or activity.

A "recombinant" nucleic acid is defined either by its method of production or its structure. In reference to its method of production, e.g., a product made by a process, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence, typically selection or production. Alternatively, it can be a nucleic acid made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude products of nature, e.g., naturally occurring mutants. Thus, for example, products made by transforming cells with any unnaturally occurring vector is encompassed, as are nucleic acids comprising sequence derived using any synthetic oligonucleotide process. Such is often done to replace a codon with a redundant codon encoding the same or a conservative amino acid, while typically introducing or removing a sequence recognition site.

Alternatively, it is performed to join together nucleic acid segments of desired functions to generate a single genetic entity comprising a desired combination of functions not found in the commonly available natural forms. Restriction enzyme

recognition sites are often the target of such artificial manipulations, but other site specific targets, e.g., promoters, DNA replication sites, regulation sequences, control sequences, or other useful features may be incorporated by design. A similar concept is intended for a recombinant, e.g., fusion, polypeptide. Specifically included are synthetic nucleic acids which, by genetic code redundancy, encode polypeptides similar to fragments of these antigens, and fusions of sequences from various different species variants.

A significant "fragment" in a nucleic acid context is a contiguous segment of at least about 17 nucleotides, generally at least about 22 nucleotides, ordinarily at least about 29 nucleotides, more often at least about 35 nucleotides, typically at least about 41 nucleotides, usually at least about 47 nucleotides, preferably at least about 55 nucleotides, and in particularly preferred embodiments will be at least about 60 or more nucleotides.

Recombinant clones derived from genomic sequences, e.g., containing introns, will be useful for transgenic studies, including, e.g., transgenic cells and organisms, and for gene therapy. See, e.g., Goodnow (1992) "Transgenic Animals" in Roitt (ed.) Encyclopedia of Immunology, Academic Press, San Diego, pp. 1502-1504; Travis (1992) Science 256:1392-1394; Kuhn, et al. (1991) Science 254:707-710; Capecchi (1989) Science 244:1288; Robertson (1987) (ed.) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Oxford; and Rosenberg (1992) J. Clinical Oncology 10:180-199.

Substantial homology in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 50% of the nucleotides, generally at least about 58%, ordinarily at least about 65%, often at least about 71%, typically at least about 77%, usually at least about 85%, preferably at least about 95 to 98% or more, and in particular embodiments, as high as about 99% or more of the

nucleotides. Alternatively, substantial homology exists when the segments will hybridize under selective hybridization conditions, to a strand, or its complement, typically using a sequence encoding a mutein.

V. Antibodies

Antibodies can be raised to portions of cytokines which bind to the muteins described herein, including species or allelic variants, and fragments thereof. Additionally, antibodies can be raised to cytokine muteins in either their active forms or in their inactive forms. Anti-idiotypic antibodies are also contemplated.

Antibodies, including binding fragments and single chain versions, against predetermined fragments of the ligands can be raised by immunization of animals with conjugates of fragments with immunogenic proteins. Monoclonal antibodies are prepared from cells secreting the desired antibody. These antibodies can be screened for binding to fragments containing sequences including the specified modifications. These monoclonal antibodies will usually bind with at least a K_D of about 1 mM, more usually at least about 300 µM, typically at least about 100 µM, more typically at least about 30 µM, preferably at least about 10 µM, and more preferably at least about 3 µM or better.

The antibodies of this invention can also be useful in diagnostic applications. See e.g., Chan (ed.) (1987) Immunology: A Practical Guide, Academic Press, Orlando, FL; Price and Newman (eds.) (1991) Principles and Practice of Immunoassay, Stockton Press, N.Y.; and Ngo (ed.) (1988) Nonisotopic Immunoassay, Plenum Press, N.Y.

Mutein fragments may be joined to other materials, particularly polypeptides, as fused or covalently joined polypeptides to be used as immunogens. A mutein or its fragments may be fused or covalently linked to a variety of immunogens, such as keyhole limpet hemocyanin, bovine serum albumin, tetanus toxoid, etc. See Microbiology, Hoeber Medical Division, Harper and Row, 1969; Landsteiner (1962) Specificity

of Serological Reactions, Dover Publications, New York; Williams, et al. (1967) Methods in Immunology and Immunochemistry, vol. 1, Academic Press, New York; and Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press, NY, for descriptions of methods of preparing polyclonal antisera.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, etc. Description of techniques for preparing such monoclonal antibodies may be found in, e.g., Stites, et al. (eds.) Basic and Clinical Immunology (4th ed.), Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.), Academic Press, New York; and particularly in Kohler and Milstein (1975) in Nature 256:495-497, which discusses one method of generating monoclonal antibodies.

Other suitable techniques involve *in vitro* exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors. See, Huse, et al. (1989) "Generation of a Large Combinatorial Library of the Immunoglobulin Repertoire in Phage Lambda," Science 246:1275-1281; and Ward, et al. (1989) Nature 341:544-546. The polypeptides and antibodies of the present invention may be used with or without modification, including chimeric or humanized antibodies. Frequently, the polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like. Patents, teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant immunoglobulins may be produced, see Cabilly, U.S. Patent No.

4,816,567; Moore, et al., U.S. Patent No. 4,642,334; and Queen, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:10029-10033.

The antibodies of this invention can also be used for affinity chromatography in isolating the protein. Columns can be prepared where the antibodies are linked to a solid support. See, e.g., Wilchek et al. (1984) Meth. Enzymol. 104:3-55.

Antibodies raised against each mutein will also be useful to raise anti-idiotypic antibodies. These will be useful in detecting or diagnosing various immunological conditions related to expression of the respective antigens.

VI. Making Agonists and Antagonists

DNA which encodes the cytokines or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or screening genomic libraries prepared from a wide variety of cell lines or tissue samples. See, e.g., Okayama and Berg (1982) Mol. Cell. Biol. 2:161-170; Gubler and Hoffman (1983) Gene 25:263-269; and Glover (ed.) (1984) DNA Cloning: A Practical Approach, IRL Press, Oxford. Suitable sequences can be obtained from GenBank.

This DNA can be mutated for expression in a wide variety of host cells for the synthesis of a full-length mutein or fragments which can in turn, e.g., be used to generate polyclonal or monoclonal antibodies; for binding studies; for construction and expression of modified molecules; and for structure/function studies.

Vectors, as used herein, comprise plasmids, viruses, bacteriophage, integratable DNA fragments, and other vehicles which enable the integration of DNA fragments into the genome of the host. See, e.g., Pouwels, et al. (1985 and Supplements) Cloning Vectors: A Laboratory Manual, Elsevier, N.Y.; Rodriguez, et al. (1988)(eds.) Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Buttersworth, Boston, MA;

For purposes of this invention, DNA sequences are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably

linked to a polypeptide if it is expressed as a preprotein or participates in directing the polypeptide to the cell membrane or in secretion of the polypeptide. A promoter is operably linked to a coding sequence if it controls the transcription of the polypeptide; a ribosome binding site is operably linked to a coding sequence if it is positioned to permit translation. Usually, operably linked means contiguous and in reading frame, however, certain genetic elements such as repressor genes are not contiguously linked but still bind to operator sequences that in turn control expression. See e.g., Rodriguez, et al., Chapter 10, pp. 205-236; Balbas and Bolivar (1990) Methods in Enzymology 185:14-37; and Ausubel, et al. (1993) Current Protocols in Molecular Biology, Greene and Wiley, NY.

Representative examples of suitable expression vectors include pCDNA1; pCD, see Okayama, et al. (1985) Mol. Cell Biol. 5:1136-1142; pMC1neo Poly-A, see Thomas, et al. (1987) Cell 51:503-512; and a baculovirus vector such as pAC 373 or pAC 610. See, e.g., Miller (1988) Ann. Rev. Microbiol. 42:177-199.

It will often be desired to express a mutein or polypeptide in a system which provides a specific or defined glycosylation pattern. See, e.g., Luckow and Summers (1988) Bio/Technology 6:47-55; and Kaufman (1990) Meth. Enzymol. 185:487-511.

The appropriate mutein, or a fragment thereof, may be engineered to be phosphatidyl inositol (PI) linked to a cell membrane, but can be removed from membranes by treatment with a phosphatidyl inositol cleaving enzyme, e.g., phosphatidyl inositol phospholipase-C. This releases the antigen in a biologically active form, and allows purification by standard procedures of protein chemistry. See, e.g., Low (1989) Biochim. Biophys. Acta 988:427-454; Tse, et al. (1985) Science 230:1003-1008; and Brunner, et al. (1991) J. Cell Biol. 114:1275-1283.

Once a particular mutein has been characterized, fragments or derivatives thereof can be prepared by conventional processes for synthesizing peptides. These include processes such as are described in Stewart and Young (1984) Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL; Bodanszky and

Bodanszky (1984) The Practice of Peptide Synthesis, Springer-Verlag, New York; and Bodanszky (1984) The Principles of Peptide Synthesis, Springer-Verlag, New York; and Villafranca (ed.) (1991) Techniques in Protein Chemistry II, Academic Press, San Diego, Ca.

VII. Uses

The present invention provides reagents which will find use in diagnostic applications as described elsewhere herein, e.g., in the general description for developmental abnormalities, or below in the description of kits for diagnosis.

The cytokine muteins, fragments thereof, and antibodies thereto, should be useful in the evaluation or quality control of recombinant production of various cytokines. They may also be useful in vitro or in vivo screening or treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g., cancerous conditions, or degenerative conditions. In particular, modulation of cytokine activities should be useful in situations where the cytokine functions have been implicated, e.g., immunological responses, inflammation, autoimmunity, abnormal proliferation, regeneration, degeneration, and atrophy of responsive cell types. For example, a disease or disorder associated with abnormal expression or abnormal signaling by a cytokine should be a likely target for treatment using an antagonist or agonist.

Other abnormal or inappropriate physiological or developmental conditions are known in each of the cell types shown to be responsive to the specified cytokines. See Berkow (ed.) The Merck Manual of Diagnosis and Therapy, Merck & Co., Rahway, N.J.; and Thorn, et al. Harrison's Principles of Internal Medicine, McGraw-Hill, N.Y. For example, neural and brain abnormalities exist in, e.g., cerebrovascular disease, CNS neoplasms, demyelinating diseases, and muscular dystrophies. Liver disorders, kidney disorders, cardiopulmonary disorders, and other problems often cause medical symptoms. These problems

may be susceptible to prevention or treatment using compositions provided herein.

For example, the IL-2 muteins would be useful in mediating immune suppression or IL-2 dependent proliferation, e.g., in certain lymphomas. IL-13 muteins would be useful in modulating IgE mediated responses and other IL-13 mediated responses. Similar uses will be found with the GM-CSF, IL-3, IL-5, IL-7, IL-9, and IL-15 muteins.

Recombinant cytokine muteins or, in some instances, antibodies can be purified and then administered to a patient. These reagents can be combined for therapeutic use with additional active or inert ingredients, e.g., in conventional pharmaceutically acceptable carriers or diluents, e.g., immunogenic adjuvants, along with physiologically innocuous stabilizers and excipients. These combinations can be sterile filtered and placed into dosage forms as by lyophilization in dosage vials or storage in stabilized aqueous preparations. This invention also contemplates use of antibodies or binding fragments thereof, including forms which are not complement binding.

The quantities of reagents necessary for effective therapy will depend upon many different factors, including means of administration, target site, physiological state of the patient, and other medicants administered. Thus, treatment dosages should be titrated to optimize safety and efficacy. Typically, dosages used in vitro may provide useful guidance in the amounts useful for <u>in situ</u> administration of these reagents. Animal testing of effective doses for treatment of particular disorders will provide further predictive indication of human dosage. Various considerations are described, e.g., in Gilman, et al. (eds.) (1990) <u>Goodman and Gilman's: The Pharmacological Bases of Therapeutics</u>, 8th Ed., Pergamon Press; and <u>Remington's Pharmaceutical Sciences</u>, 17th ed. (1990), Mack Publishing Co., Easton, Penn. Methods for administration are discussed therein and below, e.g., for oral, intravenous, intraperitoneal, or intramuscular administration, transdermal diffusion, and others.

Pharmaceutically acceptable carriers will include water, saline, buffers, and other compounds described, e.g., in the Merck Index, Merck & Co., Rahway, New Jersey. Dosage ranges would ordinarily be expected to be in amounts lower than 1 mM concentrations, typically less than about 10 μM concentrations, usually less than about 100 nM, preferably less than about 10 pM (picomolar), and most preferably less than about 1 fM (femtomolar), with an appropriate carrier. Slow release formulations, or a slow release apparatus will often be utilized for continuous administration. See, e.g., Langer (1990) Science 249:1527-1533.

These cytokine muteins may be administered directly to the host to be treated or, depending on the size of the compounds, it may be desirable to conjugate them to carrier proteins such as ovalbumin or serum albumin prior to their administration. Therapeutic formulations may be administered in any conventional dosage formulation. While it is possible for the active ingredient to be administered alone, it is preferable to present it as a pharmaceutical formulation. Formulations typically comprise at least one active ingredient, as defined above, together with one or more acceptable carriers thereof. Each carrier should be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. Formulations include those suitable for oral, rectal, nasal, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well known in the art of pharmacy. See, e.g., Gilman, et al. (eds.) (1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; Avis, et al. (eds.) (1993) Pharmaceutical Dosage Forms: Parenteral Medications, Dekker, New York; Lieberman, et al. (eds.) (1990) Pharmaceutical Dosage Forms: Tablets, Dekker, New York; and Lieberman, et al. (eds.) (1990) Pharmaceutical

Dosage Forms: Disperse Systems, Dekker, New York. The therapy of this invention may be combined with or used in association with other agents.

The muteins of this invention are particularly useful in kits and assay methods which are capable of screening compounds for binding activity to the proteins. Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds in a short period. See, e.g., Fodor, et al. (1991) Science 251:767-773, which describes means for testing of binding affinity by a plurality of defined polymers synthesized on a solid substrate.

For example, antagonists can normally be found once the ligand has been structurally defined. Testing of potential ligand analogs is now possible. In particular, new agonists and antagonists will be discovered by using screening techniques described herein. Of particular importance are compounds found to have a combined binding affinity for multiple cytokine receptors, e.g., compounds which can serve as antagonists for a plurality of cytokines.

One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant DNA molecules expressing the cytokine receptor. Cells may be isolated which express a receptor in isolation from any others. Such cells, either in viable or fixed form, can be used for standard ligand/receptor binding assays. See also, Parce, et al. (1989) Science 246:243-247; and Owicki, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:4007-4011, which describe sensitive methods to detect cellular responses.

Rational drug design may also be based upon structural studies of the molecular shapes of the agonists or antagonists and other effectors or analogs. Effectors may be other proteins which mediate other functions in response to ligand binding, or other proteins which normally interact with the receptor. One means for determining which sites interact with specific other proteins is a physical structure determination, e.g., x-ray crystallography or 2 dimensional NMR techniques. These will

provide guidance as to which amino acid residues form molecular contact regions. For a detailed description of protein structural determination, see, e.g., Blundell and Johnson (1976) Protein Crystallography, Academic Press, New York.

VIII. Kits

This invention also contemplates use of these muteins, proteins, fragments thereof, peptides, and their fusion products in a variety of diagnostic kits and methods for diagnosing the receptor interactions of a cytokine. Typically the kit will have a compartment containing either a defined mutein peptide or a reagent which recognizes one, e.g., receptor fragments or antibodies.

A kit for determining the binding affinity of a test compound to a receptor would typically comprise a test compound; a labeled compound, for example a receptor or antibody having known binding affinity for the cytokine or its mutein; a source of mutein; and a means for separating bound from free labeled compound, such as a solid phase for immobilizing the mutein. Once compounds are screened, those having suitable binding affinity to the receptor can be evaluated in suitable biological assays, as are well known in the art, to determine whether they act as agonists or antagonists to the receptor.

Antibodies, including antigen binding fragments, specific for muteins or unique fragments are useful in diagnostic applications to detect the presence of the muteins. In certain circumstances, it will be useful to quantitate amounts of muteins in a sample. Diagnostic assays may be homogeneous (without a separation step between free reagent and antigen-ligand complex) or heterogeneous (with a separation step). Various commercial assays exist, such as radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), enzyme-multiplied immunoassay technique (EMIT), substrate-labeled fluorescent immunoassay (SLFIA), and the like. See, e.g., Van Vunakis, et al. (1980) Meth Enzymol. 70:1-525; Harlow and Lane (1980) Antibodies: A Laboratory Manual, CSH

Press, NY; and Coligan, et al. (eds.) (1993) Current Protocols in Immunology, Greene and Wiley, NY.

Anti-idiotypic antibodies may have similar use to diagnose presence of antibodies against a mutein, as such may be diagnostic of various abnormal states.

Frequently, the reagents for diagnostic assays are supplied in kits, so as to optimize the sensitivity of the assay. For the subject invention, depending upon the nature of the assay, the protocol, and the label, either labeled or unlabeled antibody or receptor, or labeled mutein is provided. This is usually in conjunction with other additives, such as buffers, stabilizers, materials necessary for signal production such as substrates for enzymes, and the like. Preferably, the kit will also contain instructions for proper use and disposal of the contents after use. Typically the kit has compartments for each useful reagent. Desirably, the reagents are provided as a dry lyophilized powder, where the reagents may be reconstituted in an aqueous medium providing appropriate concentrations of reagents for performing the assay.

Any of the aforementioned constituents of the drug screening and the diagnostic assays may be used without modification or may be modified in a variety of ways. For example, labeling may be achieved by covalently or non-covalently joining a moiety which directly or indirectly provides a detectable signal. In any of these assays, the test compound, mutein, or antibodies thereto can be labeled either directly or indirectly. Possibilities for direct labeling include label groups: radiolabels such as ^{125}I, enzymes (U.S. Pat. No. 3,645,090) such as peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) capable of monitoring the change in fluorescence intensity, wavelength shift, or fluorescence polarization. Possibilities for indirect labeling include biotinylation of one constituent followed by binding to avidin coupled to one of the above label groups.

There are also numerous methods of separating the bound from the free ligand, or alternatively the bound from the free

test compound. The mutein can be immobilized on various matrixes followed by washing. Suitable matrixes include plastic such as an ELISA plate, filters, and beads. See, e.g., Coligan, et al. (eds.) (1993) Current Protocols in Immunology, Vol. 1, Chapter 2, Greene and Wiley, NY. Other suitable separation techniques include, without limitation, the fluorescein antibody magnetizable particle method described in Rattle, et al. (1984) Clin. Chem. 30:1457-1461, and the double antibody magnetic particle separation as described in U.S. Pat. No. 4,659,678.

Methods for linking proteins or their fragments to the various labels have been extensively reported in the literature and do not require detailed discussion here. Many of the techniques involve the use of activated carboxyl groups either through the use of carbodiimide or active esters to form peptide bonds, the formation of thioethers by reaction of a mercapto group with an activated halogen such as chloroacetyl, or an activated olefin such as maleimide, for linkage, or the like. Fusion proteins will also find use in these applications.

Diagnostic kits which also test for the qualitative or quantitative presence of other markers are also contemplated. Diagnosis or prognosis may depend on the combination of multiple indications used as markers. Thus, kits may test for combinations of markers. See, e.g., Viallet, et al. (1989) Progress in Growth Factor Res. 1:89-97.

All references cited herein are incorporated herein by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

The broad scope of this invention is best understood with reference to the following examples, which are not intended to limit the invention to specific embodiments.

EXAMPLES

General Methods

Some of the standard methods are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), vols 1-3, CSH Press, NY; Ausubel, et al., Biology, Greene Publishing Associates, Brooklyn, NY; or Ausubel, et al. (1987 and Supplements) Current Protocols in Molecular Biology, Greene and Wiley, New York; Innis, et al. (eds.)(1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, N.Y. Methods for protein purification include such methods as ammonium sulfate precipitation, column chromatography, electrophoresis, centrifugation, crystallization, and others. See, e.g., Ausubel, et al. (1987 and periodic supplements); Deutscher (1990) "Guide to Protein Purification" in Methods in Enzymology vol. 182, and other volumes in this series; and manufacturer's literature on use of protein purification products, e.g., Pharmacia, Piscataway, N.J., or Bio-Rad, Richmond, CA. Combination with recombinant techniques allow fusion to appropriate segments, e.g., to a FLAG sequence or an equivalent which can be fused via a protease-removable sequence. See, e.g., Hochuli (1989) Chemische Industrie 12:69-70; Hochuli (1990) "Purification of Recombinant Proteins with Metal Chelate Absorbent" in Setlow (ed.) Genetic Engineering, Principle and Methods 12:87-98, Plenum Press, N.Y.; and Crowe, et al. (1992) QIAexpress: The High Level Expression & Protein Purification System QUIAGEN, Inc., Chatsworth, CA. Cell culture techniques are described in Doyle, et al. (eds.) (1994) Cell and Tissue Culture: Laboratory Procedures, John Wiley and Sons, NY.

FACS analyses are described in Melamed, et al. (1990) Flow Cytometry and Sorting Wiley-Liss, Inc., New York, NY; Shapiro (1988) Practical Flow Cytometry Liss, New York, NY; and Robinson, et al. (1993) Handbook of Flow Cytometry Methods Wiley-Liss, New York, NY.

Substitution Analysis of cytokines.

Methods for expression of a mutein cytokine in E. coli are described in Zurawski, et al. (1986) J. Immunol. 137:3354-3360; and Zurawski and Zurawski, et al. (1988) EMBO J. 7:1061-1069. Cassette substitution mutagenesis is described in Zurawski and Zurawski (1989) EMBO J. 8:2583-2590. Preparation and biological assay of crude extracts of mutant IL-2 proteins in the presence and absence of IL-2 antagonist is described in Zurawski and Zurawski (1988) EMBO J. 7:1061-1069; and Zurawski, et al. (1992) EMBO J. 11:3905-3910. The IL-2 muteins are prototypes for similar constructs and assays for other cytokines, both for cytokines which share these receptor subunits, and other cytokines exhibiting specific structural and/or functional similarity. See, e.g., Zurawski, et al. (1993) EMBO J. 12:2663-2670; and Zurawski, et al. (1993) EMBO J. 12:5113-5119. Similar analysis or screening of defined constructs for other cytokines, e.g., IL-13 muteins, are made by similar methods.

Receptor Binding Analysis.

Receptor binding analyses for IL-2 were performed on L cells expressing mIL-2Rα the A22 cell line, as described in Zurawski and Zurawski (1992) EMBO J. 11:3905-3910. Assays used included a heterologous displacement format with labeled ligand ([^{125}I]hIL-2, IM247 from Amersham; or [^{32}P]mIL-2.P2, see Imler and Zurawski (1992) J. Biol. Chem. 267:13185-13190) at 10^{-9} M and various concentrations of purified mIL-2 or mutant mIL-2 proteins. mIL-2 proteins were purified as described by Zurawski and Zurawski (1992) EMBO J. 11:3905-3910. Data for mIL-2 and various representative mIL-2 muteins were analyzed using the Ligand computer program, see Munson and Rodbard (1980) Anal. Biochem. 107:220-239. Receptor binding analyses were also performed on L cells expressing mIL-2Rαβ, derived by cotransfection by expression plasmids for the two receptor subunits, except the labeled ligand was at 10^{-11} M.

Similar analysis is applied to other cytokines, as described. Corresponding receptor subunits for transfection into cells with no binding capacity are available from published sequences.

Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

SEQUENCE LISTING

SEQ ID NO: 1 is human IL-2 mutein 1 amino acid sequence.
SEQ ID NO: 2 is human IL-2 mutein 2 amino acid sequenc .
SEQ ID NO: 3 is human IL-2 mutein 3 amino acid sequ nc .
SEQ ID NO: 4 is human IL-13 mutein 1 amino acid sequence.
SEQ ID NO: 5 is human IL-13 mutein 2 amino acid sequence.
SEQ ID NO: 6 is mouse P600 amino acid sequence.
SEQ ID NO: 7 is human IL-7 amino acid sequence.
SEQ ID NO: 8 is human IL-9 amino acid sequence.
SEQ ID NO: 9 is a mammalian IL-15 amino acid sequence.
SEQ ID NO: 10 is mouse GM-CSF amino acid sequence.
SEQ ID NO: 11 is human GM-CSF amino acid sequence.
SEQ ID NO: 12 is human IL-3 amino acid sequence.
SEQ ID NO: 13 is human IL-5 amino acid sequence.

(1) GENERAL INFORMATION:

(i) APPLICANT: Schering Corporation

(ii) TITLE OF INVENTION: MUTEINS OF MAMMLIAN CYTOKINES

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Schering-Plough Corporation
(B) STREET: 2000 Galloping Hill Road
(C) CITY: Kenilworth
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07033-0530

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) PRIORITY APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/284,393
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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Foulke, Cynthia
(B) REGISTRATION NUMBER: 32, 364
(C) REFERENCE/DOCKET NUMBER: DX0389

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 908-298-2987
(B) TELEFAX: 908-298-5388

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1               5                   10                  15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125

Ile Ser Thr Leu Thr
    130
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1               5                   10                  15
```

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Thr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr
130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Thr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ser Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr
130

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu
1 5 10 15

Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met
20 25 30

Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu
35 40 45

Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg
50 55 60

Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser
65 70 75 80

Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys
85 90 95

Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu
1               5                   10                  15

Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met
            20                  25                  30

Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu
        35                  40                  45

Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg
    50                  55                  60

Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Phe Ser Ser
65                  70                  75                  80

Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp
                85                  90                  95

Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Gly Pro Val Pro Arg Ser Val Ser Leu Pro Leu Thr Leu Lys Glu Leu
1               5                   10                  15

Ile Glu Glu Leu Val Asn Ile Thr Gln Asp Glu Thr Pro Leu Cys Asn
            20                  25                  30

Gly Ser Met Val Trp Ser Val Asp Leu Ala Ala Gly Gly Phe Cys Val
        35                  40                  45

Ala Leu Asp Ser Leu Thr Asn Ile Ser Asn Cys Asn Ala Ile Tyr Arg
    50                  55                  60

Thr Gln Arg Ile Leu His Gly Leu Cys Asn Arg Lys Ala Pro Thr Thr
65                  70                  75                  80

Val Ser Ser Leu Pro Asp Thr Lys Ile Glu Val Ala His Phe Ile Thr
                85                  90                  95
```

Lys Leu Leu Ser Tyr Thr Lys Gln Leu Phe Arg His Gly Pro Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
20 25 30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
35 40 45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
50 55 60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
100 105 110

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
115 120 125

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
165 170 175

His

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Leu Leu Ala Met Val Leu Thr Ser Ala Leu Leu Leu Cys Ser Val
1               5                   10                  15

Ala Gly Gln Gly Cys Pro Thr Leu Ala Gly Ile Leu Asp Ile Asn Phe
            20                  25                  30

Leu Ile Asn Lys Met Gln Glu Asp Pro Ala Ser Lys Cys His Cys Ser
        35                  40                  45

Ala Asn Val Thr Ser Cys Leu Cys Leu Gly Ile Pro Ser Asp Asn Cys
    50                  55                  60

Thr Arg Pro Cys Phe Ser Glu Arg Leu Ser Gln Met Thr Asn Thr Thr
65                  70                  75                  80

Met Gln Thr Arg Tyr Pro Leu Ile Phe Ser Arg Val Lys Lys Ser Val
                85                  90                  95

Glu Val Leu Lys Asn Asn Lys Cys Pro Tyr Phe Ser Cys Glu Gln Pro
            100                 105                 110

Cys Asn Gln Thr Thr Ala Gly Asn Ala Leu Thr Phe Leu Lys Ser Leu
        115                 120                 125

Leu Glu Ile Phe Gln Lys Glu Lys Met Arg Gly Met Arg Gly Lys Ile
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Arg Ile Ser Lys Pro His L u Arg Ser Ile Ser Ile Gln Cys Tyr
1               5                   10                  15

Leu Cys Leu Leu Leu Lys Ser His Phe Leu Thr Glu Ala Gly Ile His
            20                  25                  30

Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
        35                  40                  45

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
    50                  55                  60

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65                  70                  75                  80

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
                85                  90                  95

Val Ile Ser His Glu Ser Gly Asp Thr Asp Ile His Asp Thr Val Glu
            100                 105                 110

Asn Leu Ile Ile Leu Ala Asn Asn Ile Leu Ser Ser Asn Gly Asn Ile
        115                 120                 125

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
    130                 135                 140

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145                 150                 155                 160

Thr Ser
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu
1               5                   10                  15

Ser Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His
            20                  25                  30
```

Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val
35 40 45

Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys
50 55 60

Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu
65 70 75 80

Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser
85 90 95

Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr
100 105 110

Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu
115 120 125

Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Ser Gln Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1 5 10 15

Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp
20 25 30

Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
35 40 45

Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
50 55 60

Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
65 70 75 80

Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
85 90 95

Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
100 105 110

Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg
115 120 125

Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
130 135 140

Thr Thr Leu Ser Leu Ala Ile Phe
145 150

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Arg Met Leu Leu His Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr
1               5                   10                  15

Val Tyr Ala Ile Pro Thr Glu Ile Pro Thr Ser Ala Leu Val Lys Glu
            20                  25                  30

Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu Leu Ile Ala Asn Glu
        35                  40                  45

Thr Leu Arg Ile Pro Val Pro Val His Lys Asn His Gln Leu Cys Thr
    50                  55                  60

Glu Glu Ile Phe Gln Gly Ile Gly Thr Leu Glu Ser Gln Thr Val Gln
65                  70                  75                  80

Gly Gly Thr Val Glu Arg Leu Phe Lys Asn Leu Ser Leu Ile Lys Lys
                85                  90                  95

Tyr Ile Asp Gly Gln Lys Lys Lys Cys Gly Glu Glu Arg Arg Arg Val
            100                 105                 110

Asn Gln Phe Leu Asp Tyr Leu Gln Glu Phe Leu Gly Val Met Asn Thr
        115                 120                 125

Glu Trp Ile Ile Glu Ser
    130
```

WHAT IS CLAIMED IS:

1. A mutein of a human IL-2, said mutein exhibiting both:
   1) partial cytokine agonist activity; and
   2) a substitution in the sequence at a position:
      a) between helix B and helix C; or
      b) in helix D.

2. A mutein of Claim 1, wherein said human IL-2 has a sequence selected from the group consisting of:
   1) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCqSIIS TLT;
   2) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCETADE TATIVEFLNR WITFCqSIIS TLT; and
   3) APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RpRDLISNIN VIVLELKGSE TTFMCETADE TATIVEFLNR WITFsqSIIS TLT.

3. A mutein of Claim 1, wherein said mutein:
   1) exhibits less than 80% maximal agonist activity of natural IL-2; and/or
   2) at a 1000-fold excess antagonizes cytokine agonist activity by at least about 50%.

4. A mutein of Claim 3, wherein:
   1) said position between helix B and helix C corresponds to position 82 (pro) and said substitution at position 82 (pro) is a hydrophobic amino acid, including alanine, and/or
   2) said position in helix D corresponds to position 126 (gln), and said substitution at position 126 (gln) is an acidic amino acid, including aspartic acid.

5. A mutein of Claim 1, wherein said position corresponds to position 82 (pro) and/or 126 (gln).

6. A mutein of Claim 5, wherein said substitution is a hydrophobic amino acid, including alanine, at position 82 (pro); and/or said substitution is an acidic amino acid, including aspartic acid, at position 126 (gln).

7. A mutein of Claim 5, comprising at least two substitutions, including at position 82 of alanine and at position 126 of aspartic acid.

8. A pharmaceutical composition comprising:
  1) a mutein of Claim 1, and
  2) a pharmaceutically acceptable carrier or excipient.

9. A nucleic acid encoding a mutein of Claim 1.

10. A method of antagonizing the biological activity of IL-2 on a cell, said method comprising a step of contacting said cell with a mutein of Claim 1.

11. A mutein of a cytokine selected from:
  1) a human IL-13, said mutein exhibiting both:
    a) partial agonist activity; and
    b) a substitution in the sequence at positions corresponding to:
      i) a position in helix A; and/or
      ii) a position in helix C; and
  2) a mouse P600, said mutein exhibiting both:
    a) partial agonist activity; and
    b) a substitution in the sequence at a position in helix C.

12. A mutein of Claim 11, wherein:
  a) said human IL-13 has a sequence selected from the group consisting of:
    i) GPVPPSTALR eLIEELVNIT QNQKAPLCNG SMVWSINLTA GMYCAALESL INVSGCSAIE KTQrMLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL HLKKLFREGR FN; and
    ii) GPVPPSTALR eLIEELVNIT QNQKAPLCNG SMVWSINLTA GMYCAALESL INVSGCSAIE KTQrMLSGFC PHKVSAG-FS SLHVRDTKIE VAQFVKDLLL HLKKLFREGR FN; or
  b) said mouse P600 has a sequence of: GPVPRSVSLP LTLKELIEEL SNITQDETPL CNGSMVWSVD LAAGGFCVAL DSLTNISNCN AIYRTQrILH GLCNRKAPTT VSSLPDTKIE VAHFITKLLS YTKQLFRHGP F.

13. A mutein of Claim 11, wherein said mutein:
  a) exhibits less than 80% maximal agonist activity; and/or
  b) at a 100-fold excess antagonizes cytokine activity by at least 50%.

14. A mutein of Claim 13, wherein said position of:
  1) human IL-13 in:
    a) helix A corresponds to position 11 (glu); and/or
    b) helix C corresponds to position 64 (arg); or
  2) mouse P600 in helix C corresponds to position 67 (arg).

15. A mutein of Claim 1, wherein said position of:
  1) human IL-13 in:
    a) helix A corresponds to position 11 (glu); and/or
    b) helix C corresponds to position 64 (arg); or
  2) mouse P600 in helix C corresponds to position 67 (arg).

16. A mutein of Claim 15, wherein:
  1) said substitution of human IL-13 is:
    a) an aminated amino acid, including lysine, at position 11 (glu); and/or
    b) an acidic amino acid, including aspartic acid, at position 64 (arg); or
  2) said substitution of mouse P600 is an acidic amino acid, including aspartic acid, at position 67 (arg).

17. A nucleic acid encoding a mutein of Claim 11.

18. A method of antagonizing the biological activity of IL-4 or IL-13 on a cell, said method comprising a step of contacting said cell with a mutein of Claim 11.

19. A method of analyzing human IL-13 or mouse P600, comprising measuring the antagonistic activity of a mutein of Claim 11 in an assay.

20. A mutein of a mammalian cytokine selected from the group consisting of:
  1) IL-7;
  2) IL-9; and
  3) IL-15;
said mutein exhibiting both:
  1) partial agonist activity; and
  2) a substitution in the sequence at a position corresponding to a position in:
    a) IL-7 or IL-9 in between helix B and helix C; and/or helix D; or
    b) IL-15 in helix A and/or helix C.

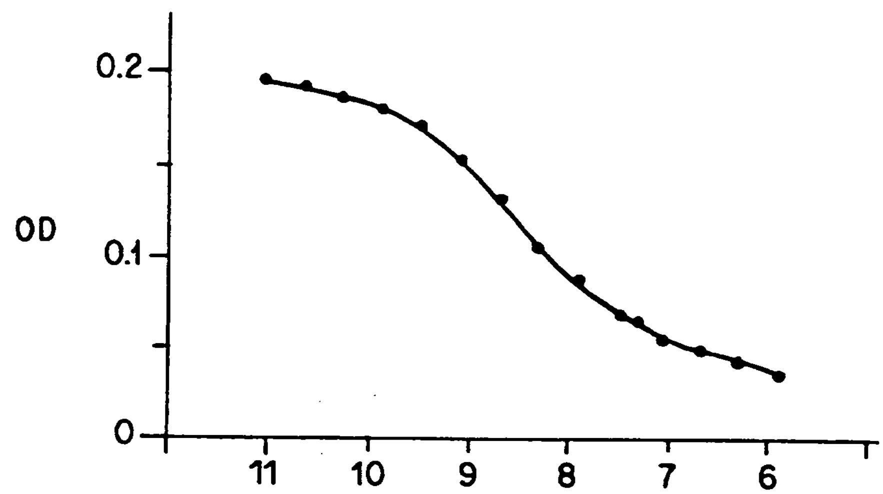
0.2
OD
0.1
0
11
10
9
8
7
6

FIG. 1A

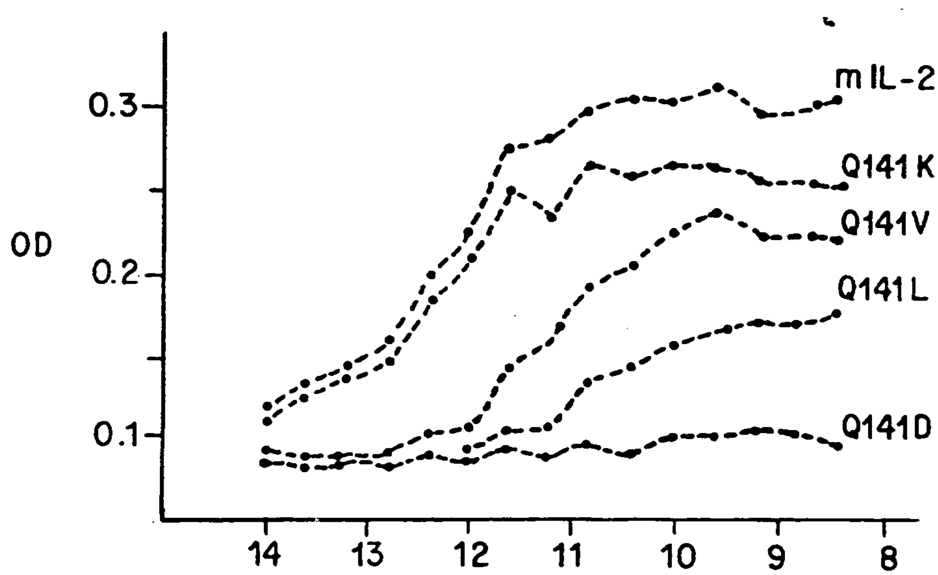
0.3
OD
0.2
0.1
mIL-2
Q141K
Q141V
Q141L
Q141D
14
13
12
11
10
9
8

FIG.1B

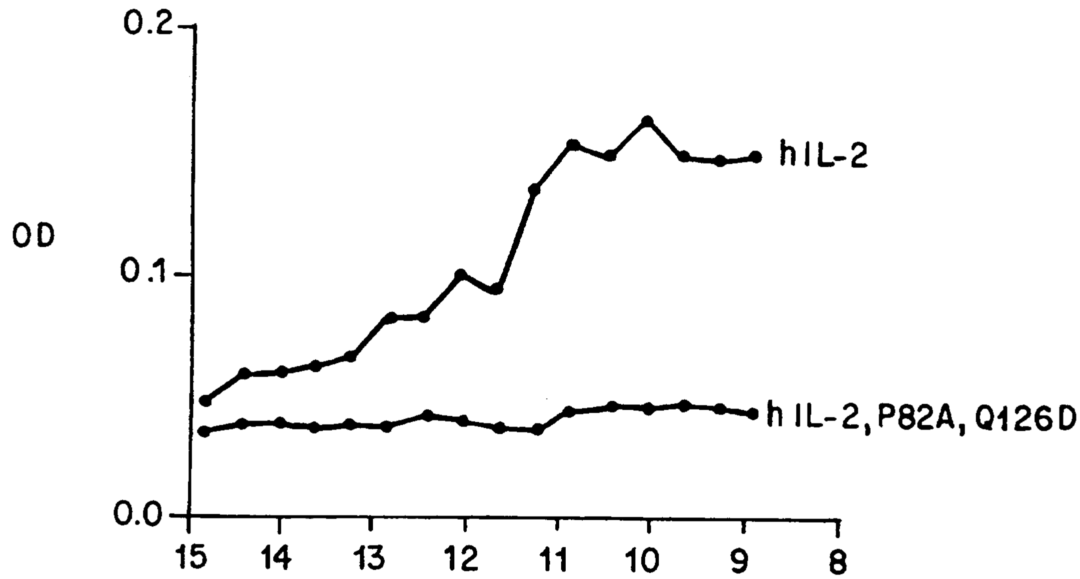
0.2
0.1
0.0
OD
hIL-2
h IL-2, P82A, Q126D
15
14
13
12
11
10
9
8

FIG. 2A

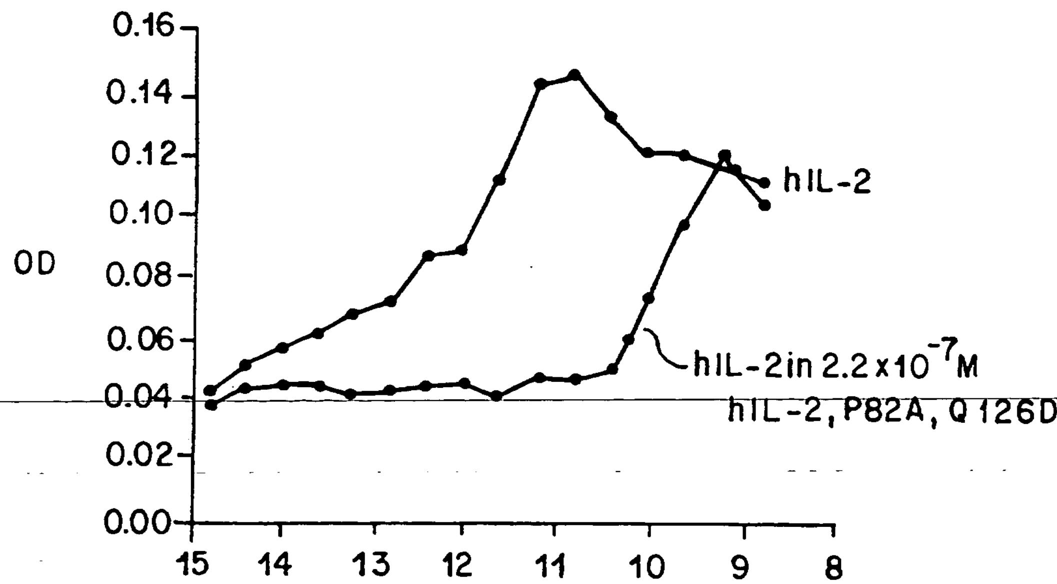
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
OD
hIL-2
hIL-2 in 2.2 x 10^{-7}M
hIL-2, P82A, Q126D
15
14
13
12
11
10
9
8

FIG. 2B

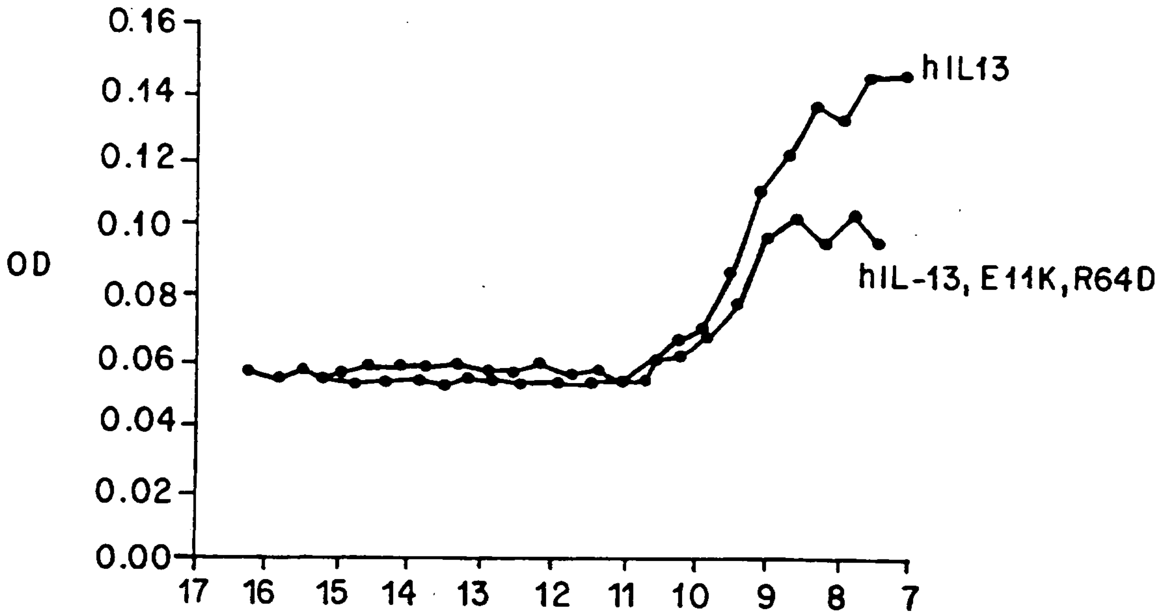
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
OD
17 16 15 14 13 12 11 10 9 8 7
hIL13
hIL-13, E11K, R64D

FIG. 3A

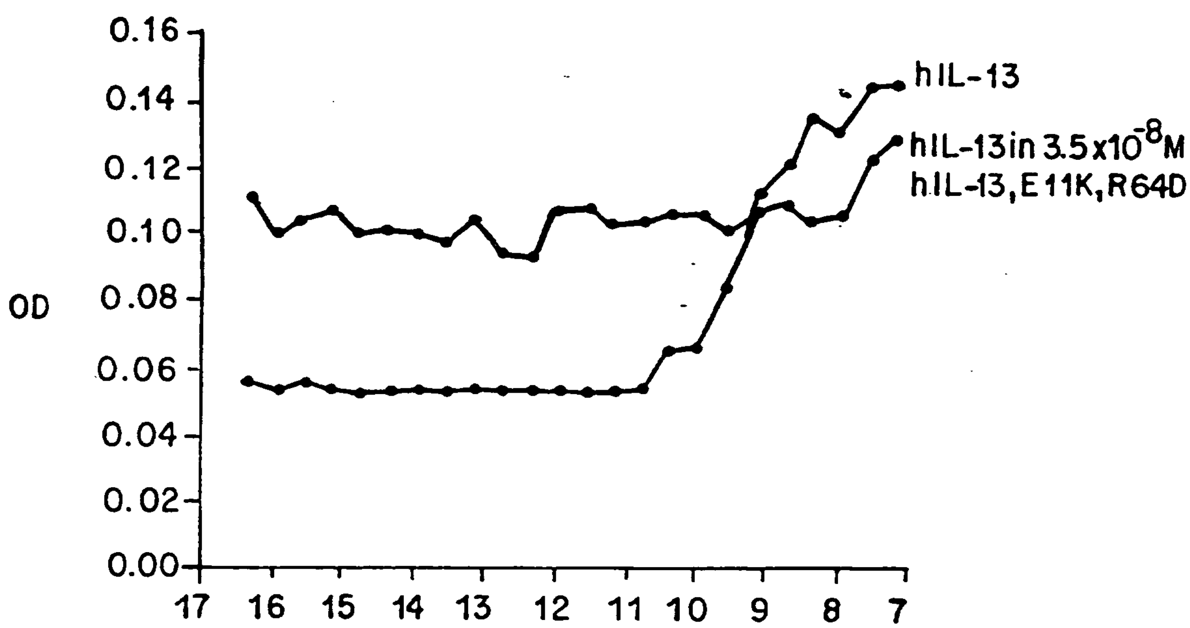
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
OD
17 16 15 14 13 12 11 10 9 8 7
hIL-13
hIL-13 in 3.5x10-8M
hIL-13, E11K, R64D

FIG. 3B

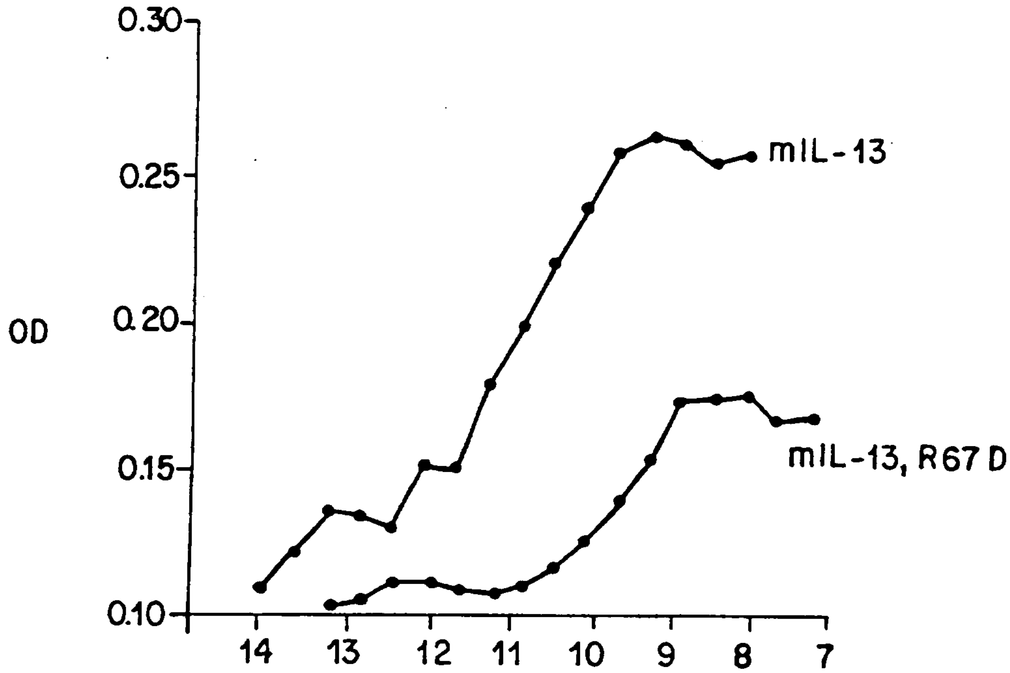
0.30
0.25
0.20
0.15
0.10
OD
14
13
12
11
10
9
8
7
mIL-13
mIL-13, R67 D

FIG. 4A

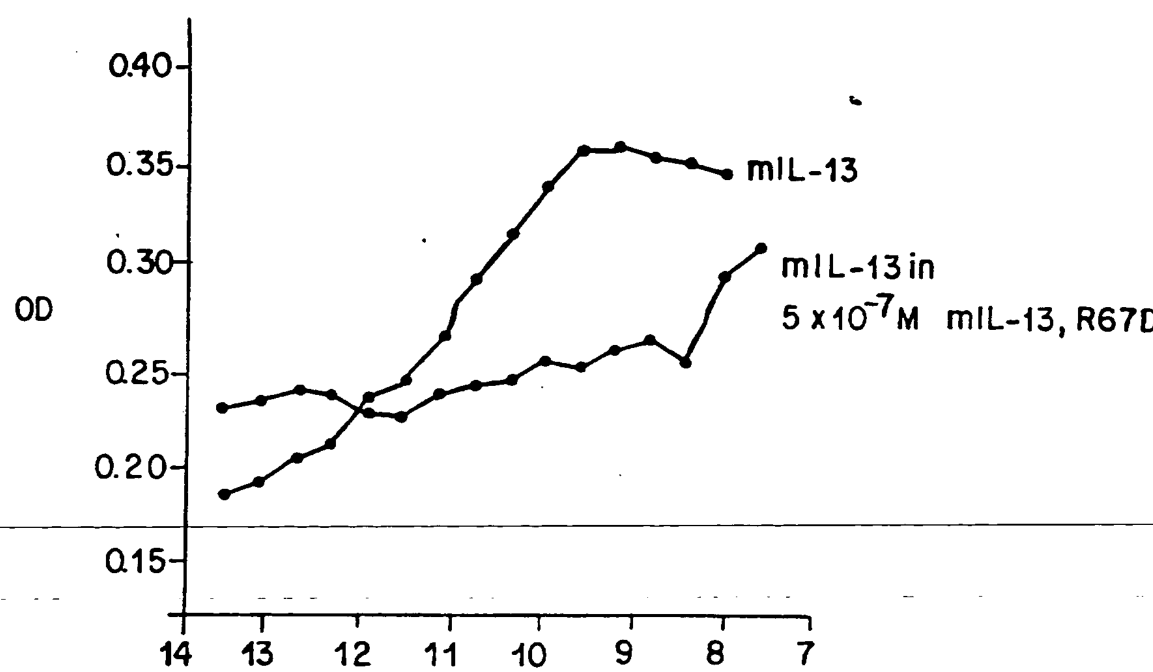
0.40
0.35
0.30
0.25
0.20
0.15
OD
14
13
12
11
10
9
8
7
mIL-13
mIL-13 in
5 x10^{-7}M mIL-13, R67D

FIG. 4B